

SEQUENCE LISTING

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<130> A21774A

<160> 30

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<212> PRT

<213> Mouse

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Leu Leu Leu Leu Arg Met Leu Trp Cys Pro Ala Asp Ala Pro Ala Arg

20

25

30

Ser Arg Leu Leu Met Glu Gly Ser Arg Glu Asp Thr Ser Gly Thr Ser

35

40

45

Ala Ala Leu Lys Thr Leu Trp Ser Pro Thr Thr Pro Val Pro Arg Thr

50

55

60

Arg Asn Ser Thr Tyr Leu Asp Glu Lys Thr Thr Gln Ile Thr Glu Lys

65

70

75

80

Cys Lys Asp Leu Gln Tyr Ser Leu Asn Ser Leu Ser Asn Lys Thr Arg

85

90

95

Arg Tyr Ser Glu Asp Asp Tyr Leu Gln Thr Ile Thr Asn Ile Gln Arg

100

105

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Cys Pro Trp Asn Arg Gln Ala Glu Glu Tyr Asp Asn Phe Arg Ala Lys

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120

125

Leu Ala Ser Cys Cys Asp Ala Ile Gln Asp Phe Val Val Ser Gln Asn

130

135

140

Asn Thr Pro Val Gly Thr Asn Met Ser Tyr Glu Val Glu Ser Lys Lys

145 150 155 160
His Ile Pro Ile Arg Glu Asn Ile Phe His Met Phe Pro Val Ser Gln
165 170 175
Pro Phe Val Asp Tyr Pro Tyr Asn Gln Cys Ala Val Val Gly Asn Gly
180 185 190
Gly Ile Leu Asn Lys Ser Leu Cys Gly Ala Glu Ile Asp Lys Ser Asp
195 200 205
Phe Val Phe Arg Cys Asn Leu Pro Pro Ile Thr Gly Ser Ala Ser Lys
210 215 220
Asp Val Gly Ser Lys Thr Asn Leu Val Thr Val Asn Pro Ser Ile Ile
225 230 235 240
Thr Leu Lys Tyr Gln Asn Leu Lys Glu Lys Lys Ala Gln Phe Leu Glu
245 250 255
Asp Ile Ser Thr Tyr Gly Asp Ala Phe Leu Leu Pro Ala Phe Ser
260 265 270
Tyr Arg Ala Asn Thr Gly Ile Ser Phe Lys Val Tyr Gln Thr Leu Lys
275 280 285
Glu Ser Lys Met Arg Gln Lys Val Leu Phe Phe His Pro Arg Tyr Leu
290 295 300
Arg His Leu Ala Leu Phe Trp Arg Thr Lys Gly Val Thr Ala Tyr Arg
305 310 315 320
Leu Ser Thr Gly Leu Met Ile Ala Ser Val Ala Val Glu Leu Cys Glu
325 330 335
Asn Val Lys Leu Tyr Gly Phe Trp Pro Phe Ser Lys Thr Ile Glu Asp
340 345 350
Thr Pro Leu Ser His His Tyr Tyr Asp Asn Met Leu Pro Lys His Gly
355 360 365

Phe His Gln Met Pro Lys Glu Tyr Ser Gln Met Leu Gln Leu His Met

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Arg Gly Ile Leu Lys Leu Gln Phe Ser Lys Cys Glu Thr Ala

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<211> 3166

<212> DNA

<213> Mouse

<400> 2

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acgcccgtgg ctcagg atg aga tcg ggg ggc acg ctg ttc gcc ctc ata 109

Met Arg Ser Gly Gly Thr Leu Phe Ala Leu Ile

1

5

10

ggc agc ctg atg ctg ctg ctc ctc ctg cgt atg ctc tgg tgc cca gcc 157

Gly Ser Leu Met Leu Leu Leu Leu Arg Met Leu Trp Cys Pro Ala

15

20

25

gac gcg cct gcc cgc tcc agg ctg ttg atg gag gga agc aga gag gac 205

Asp Ala Pro Ala Arg Ser Arg Leu Leu Met Glu Gly Ser Arg Glu Asp

30

35

40

acc agt ggt acc tca gct gca ctg aag aca ctc tgg agc ccg aca acc 253

Thr Ser Gly Thr Ser Ala Ala Leu Lys Thr Leu Trp Ser Pro Thr Thr

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50

55

ccg gta cca cgc acc agg aac agc aca tat ctg gat gag aag aca acc 301

Pro Val Pro Arg Thr Arg Asn Ser Thr Tyr Leu Asp Glu Lys Thr Thr

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65

70

75

caa ata aca gag aaa tgc aaa gat ctg caa tat agc ttg aac tct tta 349

Gln Ile Thr Glu Lys Cys Lys Asp Leu Gln Tyr Ser Leu Asn Ser Leu

80

85

90

tct aac aaa acg aga cgg tac tct gag gat gac tac ctc cag acc atc	397		
Ser Asn Lys Thr Arg Arg Tyr Ser Glu Asp Asp Tyr Leu Gln Thr Ile			
95	100	105	
aca aac ata cag aga tgc cca tgg aac cgg caa gca gaa tat gac	445		
Thr Asn Ile Gln Arg Cys Pro Trp Asn Arg Gln Ala Glu Glu Tyr Asp			
110	115	120	
aat ttt aga gca aaa ctg gct tcc tgt tgc gat gcc att caa gac ttc	493		
Asn Phe Arg Ala Lys Leu Ala Ser Cys Cys Asp Ala Ile Gln Asp Phe			
125	130	135	
gtg gtt tcc cag aac aac act cca gtg ggg act aac atg agc tac gag	541		
Val Val Ser Gln Asn Asn Thr Pro Val Gly Thr Asn Met Ser Tyr Glu			
140	145	150	155
gtg gaa agc aag aaa cac atc ccc att cga gag aac att ttc cac atg	589		
Val Glu Ser Lys Lys His Ile Pro Ile Arg Glu Asn Ile Phe His Met			
160	165	170	
ttt cca gtg tcg cag cct ttt gtg gac tat ccc tat aac cag tgt gca	637		
Phe Pro Val Ser Gln Pro Phe Val Asp Tyr Pro Tyr Asn Gln Cys Ala			
175	180	185	
gtg gtt ggt aat ggg gga att ctc aac aag tct ctc tgc gga gca gaa	685		
Val Val Gly Asn Gly Gly Ile Leu Asn Lys Ser Leu Cys Gly Ala Glu			
190	195	200	
att gat aaa tct gac ttc gtc ttc agg tgt aac ctc ccc cca atc aca	733		
Ile Asp Lys Ser Asp Phe Val Phe Arg Cys Asn Leu Pro Pro Ile Thr			
205	210	215	
ggg agc gct agt aaa gat gtt gga agc aaa aca aat ctt gtg act gtc	781		
Gly Ser Ala Ser Lys Asp Val Gly Ser Lys Thr Asn Leu Val Thr Val			
220	225	230	235

aat ccc agc att ata acc ctg aag tac cag aat ttg aag gag aag aaa			829
Asn Pro Ser Ile Ile Thr Leu Lys Tyr Gln Asn Leu Lys Glu Lys Lys			
240	245	250	
gca cag ttt ttg gag gac atc tcc acc tat gga gat gca ttc ctc ctc			877
Ala Gln Phe Leu Glu Asp Ile Ser Thr Tyr Gly Asp Ala Phe Leu Leu			
255	260	265	
ctg cca gca ttt tcc tat cgg gcc aac aca ggc atc tct ttt aaa gtc			925
Leu Pro Ala Phe Ser Tyr Arg Ala Asn Thr Gly Ile Ser Phe Lys Val			
270	275	280	
tac caa aca ctc aaa gag tca aaa atg agg caa aag gtt ctc ttc ttc			973
Tyr Gln Thr Leu Lys Glu Ser Lys Met Arg Gln Lys Val Leu Phe Phe			
285	290	295	
cat ccc agg tac ctg aga cac ctc gct ctt ttc tgg aga act aaa ggg			1021
His Pro Arg Tyr Leu Arg His Leu Ala Leu Phe Trp Arg Thr Lys Gly			
300	305	310	315
gtg act gca tac cgc ttg tcc aca ggc ttg atg att gca agt gtc gct			1069
Val Thr Ala Tyr Arg Leu Ser Thr Gly Leu Met Ile Ala Ser Val Ala			
320	325	330	
gtg gaa ctg tgt gaa aac gtg aag ctc tac gga ttc tgg cct ttc tct			1117
Val Glu Leu Cys Glu Asn Val Lys Leu Tyr Gly Phe Trp Pro Phe Ser			
335	340	345	
aag act atc gaa gac acc cca ctc agt cac cac tac tat gat aac atg			1165
Lys Thr Ile Glu Asp Thr Pro Leu Ser His His Tyr Tyr Asp Asn Met			
350	355	360	
tta cct aag cat ggt ttc cac cag atg cct aaa gaa tac agc caa atg			1213
Leu Pro Lys His Gly Phe His Gln Met Pro Lys Glu Tyr Ser Gln Met			
365	370	375	

ctc cag ctc cat atg aga gga atc ctc aaa ctg caa ttc agc aaa tgt 1261
Leu Gln Leu His Met Arg Gly Ile Leu Lys Leu Gln Phe Ser Lys Cys
370 385 390 395
gaa acg gct taa cgtttct tagaaggaga ataatttcag gaggtggagt 1310
Glu Thr Ala
398
ggatgtgtca cagcatctcc aaaaagccaa tagaagaagg cacagagaaa gcatgaatta 1370
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<211> 398

<212> PRT

<213> Human

<400> 3

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Ala Arg Ile Leu Val Glu Glu Ser Arg Glu Ala Thr His Gly Thr Pro

35 40 45

Ala Ala Leu Arg Thr Leu Arg Ser Pro Ala Thr Ala Val Pro Arg Ala

50 55 60

Thr Asn Ser Thr Tyr Leu Asn Glu Lys Ser Leu Gln Leu Thr Glu Lys

65 70 75 80

Cys Lys Asn Leu Gln Tyr Gly Ile Glu Ser Phe Ser Asn Lys Thr Lys

85 90 95

Gly Tyr Ser Glu Asn Asp Tyr Leu Gln Ile Ile Thr Asp Ile Gln Ser
100 105 110
Cys Pro Trp Lys Arg Gln Ala Glu Glu Tyr Ala Asn Phe Arg Ala Lys
115 120 125
Leu Ala Ser Cys Cys Asp Ala Val Gln Asn Phe Val Val Ser Gln Asn
130 135 140
Asn Thr Pro Val Gly Thr Asn Met Ser Tyr Glu Val Glu Ser Lys Lys
145 150 155 160
Glu Ile Pro Ile Lys Lys Asn Ile Phe His Met Phe Pro Val Ser Gln
165 170 175
Pro Phe Val Asp Tyr Pro Tyr Asn Gln Cys Ala Val Val Gly Asn Gly
180 185 190
Gly Ile Leu Asn Lys Ser Leu Cys Gly Thr Glu Ile Asp Lys Ser Asp
195 200 205
Phe Val Phe Arg Cys Asn Leu Pro Pro Thr Thr Gly Asp Val Ser Lys
210 215 220
Asp Val Gly Ser Lys Thr Asn Leu Val Thr Ile Asn Pro Ser Ile Ile
225 230 235 240
Thr Leu Lys Tyr Gly Asn Leu Lys Glu Lys Lys Ala Leu Phe Leu Glu
245 250 255
Asp Ile Ala Thr Tyr Gly Asp Ala Phe Phe Leu Pro Ala Phe Ser
260 265 270
Phe Arg Ala Asn Thr Gly Thr Ser Phe Lys Val Tyr Tyr Thr Leu Glu
275 280 285
Glu Ser Lys Ala Arg Gln Lys Val Leu Phe Phe His Pro Lys Tyr Leu
290 295 300
Lys Asp Leu Ala Leu Phe Trp Arg Thr Lys Gly Val Thr Ala Tyr Arg

305	310	315	320
Leu Ser Thr Gly Leu Met Ile Thr Ser Val Ala Val Glu Leu Cys Lys			
325	330	335	
Asn Val Lys Leu Tyr Gly Phe Trp Pro Phe Ser Lys Thr Val Glu Asp			
340	345	350	
Ile Pro Val Ser His His Tyr Tyr Asp Asn Lys Leu Pro Lys His Gly			
355	360	365	
Phe His Gln Met Pro Lys Glu Tyr Ser Gln Ile Leu Gln Leu His Met			
370	375	380	
Lys Gly Ile Leu Lys Leu Gln Phe Ser Lys Cys Glu Val Ala			
385	390	395	

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<211> 1500

<212> DNA

<213> Human

<400> 4

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atg cgg	ccg ggg	ggc gca	ctg ctc	gcc ctg	gcc agc	ctg ctg	139	
Met Arg Pro	Gly Gly	Ala Leu	Leu Ala	Leu Leu	Ala Ser	Leu Leu		
1	5	10	15					
ctg ctg	ctg cgc	ctg ctc	tgg tgc	ccg gca	gac gcg	ccc ggc	187	
Leu Leu	Leu Leu	Arg Leu	Leu Trp	Cys Pro	Ala Asp	Ala Pro	Gly Arg	
20	25	30						
gcc agg	att ctg	gtg gag	gaa agc	agg gag	gcc acc	cac ggc	acc ccc	235
Ala Arg	Ile Leu	Val Glu	Glu Ser	Arg Glu	Ala Thr	His Gly	Thr Pro	
35	40	45						

gca	gcg	ctg	agg	acg	ctc	cg	agc	ccg	g	cg	acc	g	cg	gta	ccg	cg	gc	cc	283
Ala	Ala	Leu	Arg	Thr	Leu	Arg	Ser	Pro	Ala	Thr	Ala	Val	Pro	Arg	Ala				
50				55					60										
act	aac	agc	aca	tat	ctg	aat	gag	aag	tcg	ctc	caa	ctg	acg	gag	aaa				331
Thr	Asn	Ser	Thr	Tyr	Leu	Asn	Glu	Lys	Ser	Leu	Gln	Leu	Thr	Glu	Lys				
65				70					75				80						
tgc	aaa	aat	ctg	caa	tat	ggc	att	gag	tct	ttc	tct	aac	aaa	acg	aaa				379
Cys	Lys	Asn	Leu	Gln	Tyr	Gly	Ile	Glu	Ser	Phe	Ser	Asn	Lys	Thr	Lys				
85								90					95						
ggg	tat	tca	gag	aac	gac	tac	ctt	cag	att	atc	aca	gat	ata	cag	agt				427
Gly	Tyr	Ser	Glu	Asn	Asp	Tyr	Leu	Gln	Ile	Ile	Thr	Asp	Ile	Gln	Ser				
100							105					110							
tgt	cca	tgg	aaa	cg	caa	gca	gaa	tat	gca	aat	ttt	aga	gcc	aaa					475
Cys	Pro	Trp	Lys	Arg	Gln	Ala	Glu	Glu	Tyr	Ala	Asn	Phe	Arg	Ala	Lys				
115							120					125							
ctt	gct	tcc	tgc	tgt	gat	gct	gtt	caa	aac	ttt	gtt	gtt	tct	cag	aat				523
Leu	Ala	Ser	Cys	Cys	Asp	Ala	Val	Gln	Asn	Phe	Val	Val	Ser	Gln	Asn				
130							135					140							
aac	act	cca	gtt	ggg	act	aat	atg	agt	tac	gag	gtg	gaa	agc	aaa	aaa				571
Asn	Thr	Pro	Val	Gly	Thr	Asn	Met	Ser	Tyr	Glu	Val	Glu	Ser	Lys	Lys				
145							150				155			160					
gaa	atc	cca	att	aag	aag	aac	att	ttt	cat	atg	ttt	cca	gtg	tcc	cag				619
Glu	Ile	Pro	Ile	Lys	Lys	Asn	Ile	Phe	His	Met	Phe	Pro	Val	Ser	Gln				
165								170					175						
cct	ttt	gtg	gac	tac	cct	tat	aat	cag	tgt	gca	gtg	gtc	gga	aat	ggg				667
Pro	Phe	Val	Asp	Tyr	Pro	Tyr	Asn	Gln	Cys	Ala	Val	Val	Gly	Asn	Gly				
180								185					190						

gga att ctg aat aag tct ctc tgt gga act gaa ata gat aaa tcc gac 715
Gly Ile Leu Asn Lys Ser Leu Cys Gly Thr Glu Ile Asp Lys Ser Asp
195 200 205

ttc gtt ttt agg tgt aac cta ccc cca acc aca gga gat gtt agt aaa 763
Phe Val Phe Arg Cys Asn Leu Pro Pro Thr Thr Gly Asp Val Ser Lys
210 215 220

gat gtt ggc agt aaa aca aat ctt gtg act ata aat cca agc atc ata 811
Asp Val Gly Ser Lys Thr Asn Leu Val Thr Ile Asn Pro Ser Ile Ile
225 230 235 240

act ctg aaa tat ggg aac tta aag gaa aaa aaa gcc cta ttt ttg gag 859
Thr Leu Lys Tyr Gly Asn Leu Lys Glu Lys Lys Ala Leu Phe Leu Glu
245 250 255

gac att gca acc tat gga gat gca ttt ttt ttt ctg cca gca ttt tcc 907
Asp Ile Ala Thr Tyr Gly Asp Ala Phe Phe Leu Pro Ala Phe Ser
260 265 270

ttc agg gcc aac acg ggt acc tct ttc aaa gta tac tac acg ctc gaa 955
Phe Arg Ala Asn Thr Gly Thr Ser Phe Lys Val Tyr Tyr Thr Leu Glu
275 280 285

gag tct aaa gca aga caa aag gtt cta ttt ttc cat ccc aag tac ctg 1003
Glu Ser Lys Ala Arg Gln Lys Val Leu Phe Phe His Pro Lys Tyr Leu
290 295 300

aaa gat ctg gcc ctt ttc tgg aga act aaa ggt gtg act gca tac cgc 1051
Lys Asp Leu Ala Leu Phe Trp Arg Thr Lys Gly Val Thr Ala Tyr Arg
305 310 315 320

ttg tcc acc ggc ttg atg atc aca agt gtt gca gtg gaa ctg tgt aaa 1099
Leu Ser Thr Gly Leu Met Ile Thr Ser Val Ala Val Glu Leu Cys Lys
325 330 335

aat gtg aag ctg tat gga ttc tgg ccc ttc tct aaa act gta gaa gac 1147
Asn Val Lys Leu Tyr Gly Phe Trp Pro Phe Ser Lys Thr Val Glu Asp
340 345 350
ata cct gtc agc cat cac tat tat gac aac aag cta cct aaa cat ggt 1195
Ile Pro Val Ser His His Tyr Tyr Asp Asn Lys Leu Pro Lys His Gly
355 360 365
ttc cat cag atg ccc aaa gaa tac agc cag atc ctc caa ctt cac atg 1243
Phe His Gln Met Pro Lys Glu Tyr Ser Gln Ile Leu Gln Leu His Met
370 375 380
aaa gga atc ctc aaa ctg caa ttt agc aaa tgt gaa gtc gcc taa 1288
Lys Gly Ile Leu Lys Leu Gln Phe Ser Lys Cys Glu Val Ala
385 390 395
acaaagtatc ttaaaatggg aataattta atataatgca gtaggtgatt aacaatgtct 1348
ccaaacacca aaggaggtgg ctaaagagta tttgagatg agccccaaa ttgggttga 1408
ccaaagcttc cccactcatt ttgcaatgat ggcaagtcat tcaatccttc tcattttcat 1468
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<210> 5

<211> 529

<212> PRT

<213> Human

<400> 5

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20 25 30

Ser Asn Pro Ala Glu Pro Val Pro Ser Ser Leu Ser Phe Leu Glu Thr

35 40 45

Arg Arg Leu Leu Pro Val Gln Gly Lys Gln Arg Ala Ile Met Gly Ala

50 55 60
Ala His Glu Pro Ser Pro Pro Gly Gly Leu Asp Ala Arg Gln Ala Leu
65 70 75 80
Pro Arg Ala His Pro Ala Gly Ser Phe His Ala Gly Pro Gly Asp Leu
85 90 95
Gln Lys Trp Ala Gln Ser Gln Asp Gly Phe Glu His Lys Glu Phe Phe
100 105 110
Ser Ser Gln Val Gly Arg Lys Ser Gln Ser Ala Phe Tyr Pro Glu Asp
115 120 125
Asp Asp Tyr Phe Phe Ala Ala Gly Gln Pro Gly Trp His Ser His Thr
130 135 140
Gln Gly Thr Leu Gly Phe Pro Ser Pro Gly Glu Pro Gly Pro Arg Glu
145 150 155 160
Gly Ala Phe Pro Ala Ala Gln Val Gln Arg Arg Arg Val Lys Lys Arg
165 170 175
His Arg Arg Gln Arg Arg Ser His Val Leu Glu Glu Gly Asp Asp Gly
180 185 190
Asp Arg Leu Tyr Ser Ser Met Ser Arg Ala Phe Leu Tyr Arg Leu Trp
195 200 205
Lys Gly Asn Val Ser Ser Lys Met Leu Asn Pro Arg Leu Gln Lys Ala
210 215 220
Met Lys Asp Tyr Leu Thr Ala Asn Lys His Gly Val Arg Phe Arg Gly
225 230 235 240
Lys Arg Glu Ala Gly Leu Ser Arg Ala Gln Leu Leu Cys Gln Leu Arg
245 250 255
Ser Arg Ala Arg Val Arg Thr Leu Asp Gly Thr Glu Ala Pro Phe Ser
260 265 270

Ala Leu Gly Trp Arg Arg Leu Val Pro Ala Val Pro Leu Ser Gln Leu
275 280 285
His Pro Arg Gly Leu Arg Ser Cys Ala Val Val Met Ser Ala Gly Ala
290 295 300
Ile Leu Asn Ser Ser Leu Gly Glu Glu Ile Asp Ser His Asp Ala Val
305 310 315 320
Leu Arg Phe Asn Ser Ala Pro Thr Arg Gly Tyr Glu Lys Asp Val Gly
325 330 335
Asn Lys Thr Thr Ile Arg Ile Ile Asn Ser Gln Ile Leu Thr Asn Pro
340 345 350
Ser His His Phe Ile Asp Ser Ser Leu Tyr Lys Asp Val Ile Leu Val
355 360 365
Ala Trp Asp Pro Ala Pro Tyr Ser Ala Asn Leu Asn Leu Trp Tyr Lys
370 375 380
Lys Pro Asp Tyr Asn Leu Phe Thr Pro Tyr Ile Gln His Arg Gln Arg
385 390 395 400
Asn Pro Asn Gln Pro Phe Tyr Ile Leu His Pro Lys Phe Ile Trp Gln
405 410 415
Leu Trp Asp Ile Ile Gln Glu Asn Thr Lys Glu Lys Ile Gln Pro Asn
420 425 430
Pro Pro Ser Ser Gly Phe Ile Gly Ile Leu Ile Met Met Ser Met Cys
435 440 445
Arg Glu Val His Val Tyr Glu Tyr Ile Pro Ser Val Arg Gln Thr Glu
450 455 460
Leu Cys His Tyr His Glu Leu Tyr Tyr Asp Ala Ala Cys Thr Leu Gly
465 470 475 480
Ala Tyr His Pro Leu Leu Tyr Glu Lys Leu Leu Val Gln Arg Leu Asn

485 490 495
Met Gly Thr Gln Gly Asp Leu His Arg Lys Gly Lys Val Val Leu Pro
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Gly Phe Gln Ala Val His Cys Pro Ala Pro Ser Pro Val Ile Pro His
515 520 525
Ser

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<211> 1800

<212> DNA

<213> Human

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atg aaa cca cac ttg aag caa tgg aga caa cga atg ctt ttc gga ata 223
Met Lys Pro His Leu Lys Gln Trp Arg Gln Arg Met Leu Phe Gly Ile
1 5 10 15
ttc gct tgg ggg ctc ctc ttt ttg ctg att ttc atc tac ttc acc gac 271
Phe Ala Trp Gly Leu Leu Phe Leu Leu Ile Phe Ile Tyr Phe Thr Asp
20 25 30
agc aac ccc gct gag cct gta ccc agc tcc ctc tcc ttc ctg gag acc 319
Ser Asn Pro Ala Glu Pro Val Pro Ser Ser Leu Ser Phe Leu Glu Thr
35 40 45
agg agg ctc ctg ccg gtg cag ggg aag cag cgg gcc atc atg ggc gcc 367
Arg Arg Leu Leu Pro Val Gln Gly Lys Gln Arg Ala Ile Met Gly Ala
50 55 60
gca cat gag ccc tcc ccg cct ggg ggc ctg gac gca cgc cag gcg ctg 415
Ala His Glu Pro Ser Pro Pro Gly Gly Leu Asp Ala Arg Gln Ala Leu

65 70 75 80
ccc cgc gcc cac cca gcc ggt tcc ttt cat gcg ggg cct gga gac ctg 463
Pro Arg Ala His Pro Ala Gly Ser Phe His Ala Gly Pro Gly Asp Leu
85 90 95
cag aaa tgg gcc cag tcc caa gat ggg ttt gaa cat aaa gag ttt ttt 511
Gln Lys Trp Ala Gln Ser Gln Asp Gly Phe Glu His Lys Glu Phe Phe
100 105 110
tca tcc cag gtg ggg aga aaa tct caa agt gct ttc tac ccg gag gat 559
Ser Ser Gln Val Gly Arg Lys Ser Gln Ser Ala Phe Tyr Pro Glu Asp
115 120 125
gac gac tac ttt ttt gct gct ggt cag cca ggg tgg cac agc cac act 607
Asp Asp Tyr Phe Phe Ala Ala Gly Gln Pro Gly Trp His Ser His Thr
130 135 140
cag ggg aca ttg gga ttc cct tcc ccc ggg gag cca ggc cca cgg gag 655
Gln Gly Thr Leu Gly Phe Pro Ser Pro Gly Glu Pro Gly Pro Arg Glu
145 150 155 160
ggg gct ttt ccg gct gca cag gtc cag agg agg cgg gtg aag aag agg 703
Gly Ala Phe Pro Ala Ala Gln Val Gln Arg Arg Arg Val Lys Lys Arg
165 170 175
cac cgg agg cag aga agg agc cac gtg ttg gag gag ggc gac gac ggc 751
His Arg Arg Gln Arg Arg Ser His Val Leu Glu Glu Gly Asp Asp Gly
180 185 190
gac agg ctg tac tcc tcc atg tcc agg gcc ttc ctg tac cgg ctc tgg 799
Asp Arg Leu Tyr Ser Ser Met Ser Arg Ala Phe Leu Tyr Arg Leu Trp
195 200 205
aag ggg aac gtc tct tcc aaa atg ctg aac ccg cgc ctg cag aag gcg 847
Lys Gly Asn Val Ser Ser Lys Met Leu Asn Pro Arg Leu Gln Lys Ala

210 215 220
atg aag gat tac ctg acc gcc aac aag cac ggg gtg cgc ttc cgc ggg 895
Met Lys Asp Tyr Leu Thr Ala Asn Lys His Gly Val Arg Phe Arg Gly
225 230 235 240
aag cgg gag gcc ggg ctg agc agg gca cag ctg ctg tgc cag ctg cgg 943
Lys Arg Glu Ala Gly Leu Ser Arg Ala Gln Leu Leu Cys Gln Leu Arg
245 250 255
agc cgc gcg cgc gtg cgg acg ctg gac ggc acc gag gcg ccc ttt tct 991
Ser Arg Ala Arg Val Arg Thr Leu Asp Gly Thr Glu Ala Pro Phe Ser
260 265 270
gcg ctg ggc tgg cgg cgc ctg gtg ccc gcc gtg ccc ctg agc cag ctg 1039
Ala Leu Gly Trp Arg Arg Leu Val Pro Ala Val Pro Leu Ser Gln Leu
275 280 285
cac ccc cgc ggc ctg cgc agc tgc gct gtc gtc atg tct gca ggc gca 1087
His Pro Arg Gly Leu Arg Ser Cys Ala Val Val Met Ser Ala Gly Ala
290 295 300
atc ctc aac tct tcc ttg ggc gag gaa ata gat tct cat gat gcg gtt 1135
Ile Leu Asn Ser Ser Leu Gly Glu Glu Ile Asp Ser His Asp Ala Val
305 310 315 320
ttg aga ttt aac tct gct cct aca cgt ggt tat gag aaa gat gtt ggg 1183
Leu Arg Phe Asn Ser Ala Pro Thr Arg Gly Tyr Glu Lys Asp Val Gly
325 330 335
aat aaa acc acc ata cgc atc att aat tcg cag att ctg acc aac ccc 1231
Asn Lys Thr Thr Ile Arg Ile Ile Asn Ser Gln Ile Leu Thr Asn Pro
340 345 350
agc cat cac ttc att gac agt tca ctg tat aaa gac gtc att ttg gtg 1279
Ser His His Phe Ile Asp Ser Ser Leu Tyr Lys Asp Val Ile Leu Val

355 360 365
gcc tgg gac cct gcc cca tat tcc gca aat ctt aac ctg tgg tac aaa 1327
Ala Trp Asp Pro Ala Pro Tyr Ser Ala Asn Leu Asn Leu Trp Tyr Lys
370 375 380
aaa ccg gat tac aac ctg ttc act cca tat att cag cat cgt cag aga 1375
Lys Pro Asp Tyr Asn Leu Phe Thr Pro Tyr Ile Gln His Arg Gln Arg
385 390 395 400
aac cca aat cag cca ttt tac att ctt cat cct aaa ttt ata tgg cag 1423
Asn Pro Asn Gln Pro Phe Tyr Ile Leu His Pro Lys Phe Ile Trp Gln
405 410 415
ctc tgg gat att atc cag gag aac act aaa gag aag att caa cca aac 1471
Leu Trp Asp Ile Ile Gln Glu Asn Thr Lys Glu Lys Ile Gln Pro Asn
420 425 430
cca cca tct tct ggt ttc att gga atc ctc atc atg atg tcc atg tgc 1519
Pro Pro Ser Ser Gly Phe Ile Gly Ile Leu Ile Met Met Ser Met Cys
435 440 445
aga gag gtg cac gtg tat gaa tat atc cca tcc gtg cgg cag acg gag 1567
Arg Glu Val His Val Tyr Glu Tyr Ile Pro Ser Val Arg Gln Thr Glu
450 455 460
ctg tgc cac tac cac gag ctg tac tac gac gca gcc tgc acc ctc ggg 1615
Leu Cys His Tyr His Glu Leu Tyr Tyr Asp Ala Ala Cys Thr Leu Gly
465 470 475 480
gcg tac cac cca cta ctc tat gag aag ctc ctg gtg cag cgc ctg aac 1663
Ala Tyr His Pro Leu Leu Tyr Glu Lys Leu Leu Val Gln Arg Leu Asn
485 490 495
atg ggc acg cag ggg gat ttg cat cgc aag ggc aag gtg gtt ctt cct 1711
Met Gly Thr Gln Gly Asp Leu His Arg Lys Gly Lys Val Val Leu Pro

500 505 510
ggc ttc cag gcg gtg cac tgc cct gca cca agt cca gtc att cca cac 1759
Gly Phe Gln Ala Val His Cys Pro Ala Pro Ser Pro Val Ile Pro His
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Ser

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<213> Mouse
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Phe Val Trp Gly Leu Leu Phe Leu Ala Ile Phe Ile Tyr Phe Thr Asn
20 25 30
Ser Asn Pro Ala Ala Pro Met Pro Ser Ser Phe Ser Phe Leu Glu Ser
35 40 45
Arg Gly Leu Leu Pro Leu Gln Gly Lys Gln Arg Val Ile Met Gly Ala
50 55 60
Leu Gln Glu Pro Ser Leu Pro Arg Ser Leu Asp Ala Ser Lys Val Leu
65 70 75 80
Leu Asp Ser His Pro Glu Asn Pro Phe His Pro Trp Pro Gly Asp Pro
85 90 95
Gln Lys Trp Asp Gln Ala Pro Asn Gly Phe Asp Asn Gly Asp Glu Phe
100 105 110
Phe Thr Ser Gln Val Gly Arg Lys Ser Gln Ser Ala Phe Tyr Pro Glu
115 120 125
Glu Asp Ser Tyr Phe Phe Val Ala Asp Gln Pro Glu Leu Tyr His His

130 135 140
Arg Gln Gly Ala Leu Glu Leu Pro Ser Pro Gly Glu Thr Ser Trp Arg
145 150 155 160
Ser Gly Pro Val Gln Pro Lys Gln Lys Leu Leu His Pro Arg Arg Gly
165 170 175
Ser Leu Pro Glu Glu Ala Tyr Asp Ser Asp Met Leu Ser Ala Ser Met
180 185 190
Ser Arg Ala Phe Leu Tyr Arg Leu Trp Lys Gly Ala Val Ser Ser Lys
195 200 205
Met Leu Asn Pro Arg Leu Gln Lys Ala Met Arg Tyr Tyr Met Ser Phe
210 215 220
Asn Lys His Gly Val Arg Phe Arg Arg Arg Gly Arg Arg Glu Ala Thr
225 230 235 240
Arg Thr Gly Pro Glu Leu Leu Cys Glu Met Arg Arg Arg Val Arg Val
245 250 255
Arg Thr Leu Asp Gly Arg Glu Ala Pro Phe Ser Gly Leu Gly Trp Arg
260 265 270
Pro Leu Val Pro Gly Val Pro Leu Ser Gln Leu His Pro Arg Gly Leu
275 280 285
Ser Ser Cys Ala Val Val Met Ser Ala Gly Ala Ile Leu Asn Ser Ser
290 295 300
Leu Gly Glu Glu Ile Asp Ser His Asp Ala Val Leu Arg Phe Asn Ser
305 310 315 320
Ala Pro Thr Arg Gly Tyr Glu Lys Asp Val Gly Asn Lys Thr Thr Val
325 330 335
Arg Ile Ile Asn Ser Gln Ile Leu Ala Asn Pro Ser His His Phe Ile
340 345 350

Asp Ser Ala Leu Tyr Lys Asp Val Ile Leu Val Ala Trp Asp Pro Ala
355 360 365
Pro Tyr Ser Ala Asn Leu Asn Leu Trp Tyr Lys Lys Pro Asp Tyr Asn
370 375 380
Leu Phe Thr Pro Tyr Ile Gln His Arg Arg Lys Tyr Pro Thr Gln Pro
385 390 395 400
Phe Tyr Ile Leu His Pro Lys Phe Ile Trp Gln Leu Trp Asp Ile Ile
405 410 415
Gln Glu Asn Thr Arg Glu Lys Ile Gln Pro Asn Pro Pro Ser Ser Gly
420 425 430
Phe Ile Gly Ile Leu Ile Met Met Ser Met Cys Lys Glu Val His Val
435 440 445
Tyr Glu Tyr Ile Pro Ser Val Arg Gln Thr Glu Leu Cys His Tyr His
450 455 460
Glu Leu Tyr Tyr Asp Ala Ala Cys Thr Leu Gly Ala Tyr His Pro Leu
465 470 475 480
Leu Tyr Glu Lys Leu Leu Val Gln Arg Leu Asn Thr Gly Thr Gln Ala
485 490 495
Asp Leu His His Lys Gly Lys Val Val Leu Pro Gly Phe Gln Thr Leu
500 505 510
Arg Cys Pro Val Thr Ser Pro Asn Asn Thr His Ser
515 520

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<212> DNA
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1 5 10 15
ttt gtt tgg ggg ctc ctc ttt ttg gca att ttc atc tac ttc acc aac 98
Phe Val Trp Gly Leu Leu Phe Leu Ala Ile Phe Ile Tyr Phe Thr Asn
20 25 30
agc aat cct gcg gca cct atg ccc agc tcc ttt tcc ttc ctg gag agc 146
Ser Asn Pro Ala Ala Pro Met Pro Ser Ser Phe Ser Phe Leu Glu Ser
35 40 45
cgt ggg ctc ctg cct cta cag ggc aag cag cgg gtc atc atg ggc gct 194
Arg Gly Leu Leu Pro Leu Gln Gly Lys Gln Arg Val Ile Met Gly Ala
50 55 60
ttg cag gaa ccc tct ttg ccc aga agt ttg gat gca agc aaa gtg ctt 242
Leu Gln Glu Pro Ser Leu Pro Arg Ser Leu Asp Ala Ser Lys Val Leu
65 70 75 80
ctg gac agc cac cct gag aac cct ttc cac cct tgg cct ggg gac cca 290
Leu Asp Ser His Pro Glu Asn Pro Phe His Pro Trp Pro Gly Asp Pro
85 90 95
cag aaa tgg gat cag gcc cca aat ggc ttt gac aat ggg gat gag ttt 338
Gln Lys Trp Asp Gln Ala Pro Asn Gly Phe Asp Asn Gly Asp Glu Phe
100 105 110
ttt aca tcc cag gtt ggg agg aaa tca caa agc gct ttc tat ccc gag 386
Phe Thr Ser Gln Val Gly Arg Lys Ser Gln Ser Ala Phe Tyr Pro Glu
115 120 125
gaa gat agc tat ttt ttt gtt gcg gat cag cct gag ttg tac cac cac 434
Glu Asp Ser Tyr Phe Phe Val Ala Asp Gln Pro Glu Leu Tyr His His
130 135 140

agg cag ggt gca ctg gag ctg cca tct cca ggg gag aca tca tgg cga 482
Arg Gln Gly Ala Leu Glu Leu Pro Ser Pro Gly Glu Thr Ser Trp Arg
145 150 155 160
tca gga cct gtt cag ccc aag cag aag ctg ctt cac cca agg cga ggc 530
Ser Gly Pro Val Gln Pro Lys Gln Lys Leu Leu His Pro Arg Arg Gly
165 170 175
agc ttg cct gag gaa gcc tat gac agc gac atg ctg tca gcc tcc atg 578
Ser Leu Pro Glu Glu Ala Tyr Asp Ser Asp Met Leu Ser Ala Ser Met
180 185 190
tcg aga gcc ttc ctg tac cgg ctc tgg aag ggg gcc gtg tcc tct aag 626
Ser Arg Ala Phe Leu Tyr Arg Leu Trp Lys Gly Ala Val Ser Ser Lys
195 200 205
atg ttg aac ccg cgc ctg cag aag gcc atg cgt tac tac atg tcc ttc 674
Met Leu Asn Pro Arg Leu Gln Lys Ala Met Arg Tyr Tyr Met Ser Phe
210 215 220
aac aag cat ggt gtg cgc ttc cgc agg cgg ggt cgg cgt gaa gct aca 722
Asn Lys His Gly Val Arg Phe Arg Arg Gly Arg Arg Glu Ala Thr
225 230 235 240
cgt aca ggg ccg gag ctg ctg tgt gag atg cgc aga cgt gtg cgt gtg 770
Arg Thr Gly Pro Glu Leu Leu Cys Glu Met Arg Arg Val Arg Val
245 250 255
cgc acg ttg gac ggc aga gag gcg ccc ttc tcg ggg ctg ggc tgg cgg 818
Arg Thr Leu Asp Gly Arg Glu Ala Pro Phe Ser Gly Leu Gly Trp Arg
260 265 270
cct ctg gta cca ggt gta cct ctg agc cag ttg cac ccg cgc ggt ctg 866
Pro Leu Val Pro Gly Val Pro Leu Ser Gln Leu His Pro Arg Gly Leu
275 280 285

agc agc tgc gca gtt gtc atg tct gcc ggt gcc atc ctg aac tcc tcc 914
Ser Ser Cys Ala Val Val Met Ser Ala Gly Ala Ile Leu Asn Ser Ser
290 295 300
ttg ggg gag gaa atc gat tct cat gat gca gtt ttg aga ttt aac tct 962
Leu Gly Glu Glu Ile Asp Ser His Asp Ala Val Leu Arg Phe Asn Ser
305 310 315 320
gcc cct acc cgt ggc tac gag aaa gat gtc gga aat aaa acc aca gta 1010
Ala Pro Thr Arg Gly Tyr Glu Lys Asp Val Gly Asn Lys Thr Thr Val
325 330 335
cgc atc att aat tct cag att ctg gcc aac ccc agc cat cac ttc att 1058
Arg Ile Ile Asn Ser Gln Ile Leu Ala Asn Pro Ser His His Phe Ile
340 345 350
gac agt gct tta tat aaa gat gtt atc ctg gta gcc tgg gat cct gct 1106
Asp Ser Ala Leu Tyr Lys Asp Val Ile Leu Val Ala Trp Asp Pro Ala
355 360 365
cct tat tct gcc aat ctt aac ctg tgg tat aag aag cca gat tac aac 1154
Pro Tyr Ser Ala Asn Leu Asn Leu Trp Tyr Lys Pro Asp Tyr Asn
370 375 380
ctt ttc act cca tat atc cag cat cgc cgg aaa tac ccg act cag cca 1202
Leu Phe Thr Pro Tyr Ile Gln His Arg Arg Lys Tyr Pro Thr Gln Pro
385 390 395 400
ttt tac att ctt cac ccc aag ttc ata tgg cag ctt tgg gac att atc 1250
Phe Tyr Ile Leu His Pro Lys Phe Ile Trp Gln Leu Trp Asp Ile Ile
405 410 415
cag gag aat aca agg gag aag ata cag ccc aac cca cca tct tct ggt 1298
Gln Glu Asn Thr Arg Glu Lys Ile Gln Pro Asn Pro Pro Ser Ser Gly
420 425 430

ttt att gga atc ctc atc atg atg tcc atg tgt aaa gag gtg cac gtg 1346
Phe Ile Gly Ile Leu Ile Met Met Ser Met Cys Lys Glu Val His Val
435 440 445
tat gag tac atc cca tct gtt cga cag aca gag ctt tgc cac tac cat 1394
Tyr Glu Tyr Ile Pro Ser Val Arg Gln Thr Glu Leu Cys His Tyr His
450 455 460
gag ctg tac tac gac gca gcc tgc acc ttg ggg gcc tac cac cca ctg 1442
Glu Leu Tyr Tyr Asp Ala Ala Cys Thr Leu Gly Ala Tyr His Pro Leu
465 470 475 480
ctc tat gaa aag cta ctg gtg cag cgc ctt aac aca ggc acc cag gca 1490
Leu Tyr Glu Lys Leu Leu Val Gln Arg Leu Asn Thr Gly Thr Gln Ala
485 490 495
gac ttg cat cac aag ggc aag gta gtc ttg cca ggc ttc cag acc ctt 1538
Asp Leu His His Lys Gly Lys Val Val Leu Pro Gly Phe Gln Thr Leu
500 505 510
cggttgt cca gta acc agc ccc aac aat aca cat tct taa 1577
Arg Cys Pro Val Thr Ser Pro Asn Asn Thr His Ser
515 520
aatggaaactc ttggaaactg atgtgcaata aggt 1611

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<220>
<223> Description of Artificial Sequence: Synthetic DNA
<400> 9
cttttctgga gaactaaagg 20
<210> 10

<211> 20
<212> DNA
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<223> Description of Artificial Sequence: Synthetic DNA
<400> 10
aattgcagtt tgaggattcc 20

<210> 11
<211> 20
<212> DNA
<213> Artificial Sequence
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<223> Description of Artificial Sequence: Synthetic DNA
<400> 11
tggctcagga tgagatcggg 20

<210> 12
<211> 22
<212> DNA
<213> Artificial Sequence
<220>
<223> Description of Artificial Sequence: Synthetic DNA
<400> 12
tactagcgct ccctgtgatt gg 22

<210> 13
<211> 30
<212> DNA
<213> Artificial Sequence
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<223> Description of Artificial Sequence: Synthetic DNA
<400> 13
tgctctcgag cccagccgac gcgcctgcc 30

<210> 14
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caattgacat atctgaatga gaagtcgctc 30

<210> 16
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<400> 16
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<210> 17
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<400> 17
ccagtgtccc agcctttgt 20

<210> 18
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<212> DNA
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<400> 18
tgagtgggga agctttggtc 20

<210> 19
<211> 30
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<400> 19
gacaatgggg atgagtttt tacatccag 30

<210> 20
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cgatttcctc ccccaaggag gagttcagg 29

<210> 21
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<210> 22

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<210> 23
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<400> 23
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<210> 24
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<400> 24
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<210> 25
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<400> 25
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<210> 26
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<212> DNA
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<400> 26

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<212> DNA
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<210> 28
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<400> 29

agacgtcatt ttgggtggcct ggg 23

<210> 30
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ttaagagtgt ggaatgactg g

21